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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/875,363

DATE: 06/21/2001

TIME: 17:26:15

Input Set : A:\10448-060001.TXT

Output Set: N:\CRF3\06212001\I875363.raw

4 <110> APPLICANT: Curtis, Rory A.J.
6 <120> TITLE OF INVENTION: 56201, A NOVEL HUMAN SODIUM ION CHANNEL
7 FAMILY MEMBER AND USES THEREOF
10 <130> FILE REFERENCE: 10448-060001
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/875,363
C--> 12 <141> CURRENT FILING DATE: 2001-06-05
12 <150> PRIOR APPLICATION NUMBER: US 60/209,238
13 <151> PRIOR FILING DATE: 2000-06-05
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1356
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (70)...(1263)
28 <400> SEQUENCE: 1
29 ggaaatccc taagcagaga ttttctgttg gatgctaaaa gcaaggaata aaagttgaaa 60
30 atttggaata atg tct caa cac cgt cac cag cgc cac tcg aga gtc att tct 111
31 Met Ser Gln His Arg His Gln Arg His Ser Arg Val Ile Ser
32 1 5 10
34 agt tca cca gtt gac act aca tcg gtg gga ttt tgc cca aca ttc aag 159
35 Ser Ser Pro Val Asp Thr Thr Ser Val Gly Phe Cys Pro Thr Phe Lys
36 15 20 25 30
38 aaa ttt aag agg aac gat gat gaa tgt cgg gca ttt gtg aag aga gtc 207
39 Lys Phe Lys Arg Asn Asp Asp Glu Cys Arg Ala Phe Val Lys Arg Val
40 35 40 45
42 ata atg agc cgt ttc ttt aag ata att atg att agc act gtc aca tcg 255
43 Ile Met Ser Arg Phe Phe Lys Ile Ile Met Ile Ser Thr Val Thr Ser
44 50 55 60
46 aat gcg ttt ttt atg gcc ttg tgg acc agt tat gac ata agg tac cgc 303
47 Asn Ala Phe Phe Met Ala Leu Trp Thr Ser Tyr Asp Ile Arg Tyr Arg
48 65 70 75
50 ttg ttc aga ctt ctt gag ttc tcg gag atc ttc ttt gtg tcc atc tgc 351
51 Leu Phe Arg Leu Leu Glu Phe Ser Glu Ile Phe Phe Val Ser Ile Cys
52 80 85 90
54 aca tct gag ttg tcc atg aag gtc tat gtg gac ccc atc aac tac tgg 399
55 Thr Ser Glu Leu Ser Met Lys Val Tyr Val Asp Pro Ile Asn Tyr Trp
56 95 100 105 110
58 aag aac ggc tac aac ctg ctg gat gtg atc att atc atc gtt atg ttt 447
59 Lys Asn Gly Tyr Asn Leu Leu Asp Val Ile Ile Ile Ile Val Met Phe
60 115 120 125
62 tta ccc tat gcc ctc cgc cag ctc atg ggc aaa cag ttc act tac ctg 495
63 Leu Pro Tyr Ala Leu Arg Gln Leu Met Gly Lys Gln Phe Thr Tyr Leu
64 130 135 140
66 tat atc gct gat ggc atg cag tcc ctg cgc atc ctc aag ctt atc ggc 543

ENTERED

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67 Tyr Ile Ala Asp Gly Met Gln Ser Leu Arg Ile Leu Lys Leu Ile Gly
68          145          150          155
70 tat agc cag ggc atc cgg acg ctg atc acc gcc gtg ggg cag aca gtc      591
71 Tyr Ser Gln Gly Ile Arg Thr Leu Ile Thr Ala Val Gly Gln Thr Val
72      160          165          170
74 tac acc gtg gcc tct gtg ctc ctc ctg ctc ttc ctc atg tac atc      639
75 Tyr Thr Val Ala Ser Val Leu Leu Leu Leu Phe Leu Leu Met Tyr Ile
76 175          180          185          190
78 ttc gct atc ttg ggc ttc tgc ctg ttt gga tct cca gac aat ggt gac      687
79 Phe Ala Ile Leu Gly Phe Cys Leu Phe Gly Ser Pro Asp Asn Gly Asp
80          195          200          205
82 cat gat aac tgg ggg aac ctg gct gca gct ttt ttc acc ctc ttc agc      735
83 His Asp Asn Trp Gly Asn Leu Ala Ala Ala Phe Phe Thr Leu Phe Ser
84          210          215          220
86 ttg gcc acg gtt gat ggc tgg aca gac ctg cag aag cag ttg gac aat      783
87 Leu Ala Thr Val Asp Gly Trp Thr Asp Leu Gln Lys Gln Leu Asp Asn
88          225          230          235
90 cgg gaa ttt gct ttg agc cgg gca ttc acc atc atc ttc atc ttg ctc      831
91 Arg Glu Phe Ala Leu Ser Arg Ala Phe Thr Ile Ile Phe Ile Leu Leu
92      240          245          250
94 gcc tct ttc atc ttc ctc aac atg ttc gtg ggt gtg atg atc atg cac      879
95 Ala Ser Phe Ile Phe Leu Asn Met Phe Val Gly Val Met Ile Met His
96 255          260          265          270
98 aca gag gac tcc atc aga aag ttt gag cga gag ctg atg ttg gag cag      927
99 Thr Glu Asp Ser Ile Arg Lys Phe Glu Arg Glu Leu Met Leu Glu Gln
100          275          280          285
102 cag gag atg ctc atg gga gag aag cag gtg att ctg cag cgg cag cag      975
103 Gln Glu Met Leu Met Gly Glu Lys Gln Val Ile Leu Gln Arg Gln Gln
104          290          295          300
106 gag gag atc agc agg ctg atg cac ata cag aaa aat gct gac tgc aca      1023
107 Glu Glu Ile Ser Arg Leu Met His Ile Gln Lys Asn Ala Asp Cys Thr
108          305          310          315
110 agt ttc agt gag ctg gtg gag aac ttt aag aag acc ttg agc cac act      1071
111 Ser Phe Ser Glu Leu Val Glu Thr Asn Phe Lys Lys Thr Leu Ser His Thr
112          320          325          330
114 gac cca atg gtc ttg gat gat ttt ggc act agc tta ccc ttc atc gat      1119
115 Asp Pro Met Val Leu Asp Asp Phe Gly Thr Ser Leu Pro Phe Ile Asp
116 335          340          345          350
118 atc tac ttt tcc act ctg gac tac cag gac aca act gtc cac aag ctt      1167
119 Ile Tyr Phe Ser Thr Leu Asp Tyr Gln Asp Thr Thr Val His Lys Leu
120          355          360          365
122 caa gag ctg tac tat gag atc gtg cat gtg ctg agc cta atg ctg gaa      1215
123 Gln Glu Leu Tyr Tyr Glu Ile Val His Val Leu Ser Leu Met Leu Glu
124          370          375          380
126 gac ttg ccc cag gag aag ccc cag tcc ttg gaa aag gtg gat gag aag      1263
127 Asp Leu Pro Gln Glu Lys Pro Gln Ser Leu Glu Lys Val Asp Glu Lys
128          385          390          395
130 tagctgggca tggggcaccc atgtgccgag agccttgacag accatgacag gtcctatta      1323
131 aacacaggct ttctgaaaaa aaaaaaaaaa aaa      1356

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```

133 <210> SEQ ID NO: 2
134 <211> LENGTH: 398
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 2
139 Met Ser Gln His Arg His Gln Arg His Ser Arg Val Ile Ser Ser Ser
140 1 5 10 15
141 Pro Val Asp Thr Thr Ser Val Gly Phe Cys Pro Thr Phe Lys Lys Phe
142 20 25 30
143 Lys Arg Asn Asp Asp Glu Cys Arg Ala Phe Val Lys Arg Val Ile Met
144 35 40 45
145 Ser Arg Phe Phe Lys Ile Ile Met Ile Ser Thr Val Thr Ser Asn Ala
146 50 55 60
147 Phe Phe Met Ala Leu Trp Thr Ser Tyr Asp Ile Arg Tyr Arg Leu Phe
148 65 70 75 80
149 Arg Leu Leu Glu Phe Ser Glu Ile Phe Phe Val Ser Ile Cys Thr Ser
150 85 90 95
151 Glu Leu Ser Met Lys Val Tyr Val Asp Pro Ile Asn Tyr Trp Lys Asn
152 100 105 110
153 Gly Tyr Asn Leu Leu Asp Val Ile Ile Ile Ile Val Met Phe Leu Pro
154 115 120 125
155 Tyr Ala Leu Arg Gln Leu Met Gly Lys Gln Phe Thr Tyr Leu Tyr Ile
156 130 135 140
157 Ala Asp Gly Met Gln Ser Leu Arg Ile Leu Lys Leu Ile Gly Tyr Ser
158 145 150 155 160
159 Gln Gly Ile Arg Thr Leu Ile Thr Ala Val Gly Gln Thr Val Tyr Thr
160 165 170 175
161 Val Ala Ser Val Leu Leu Leu Leu Phe Leu Leu Met Tyr Ile Phe Ala
162 180 185 190
163 Ile Leu Gly Phe Cys Leu Phe Gly Ser Pro Asp Asn Gly Asp His Asp
164 195 200 205
165 Asn Trp Gly Asn Leu Ala Ala Ala Phe Phe Thr Leu Phe Ser Leu Ala
166 210 215 220
167 Thr Val Asp Gly Trp Thr Asp Leu Gln Lys Gln Leu Asp Asn Arg Glu
168 225 230 235 240
169 Phe Ala Leu Ser Arg Ala Phe Thr Ile Ile Phe Ile Leu Leu Ala Ser
170 245 250 255
171 Phe Ile Phe Leu Asn Met Phe Val Gly Val Met Ile Met His Thr Glu
172 260 265 270
173 Asp Ser Ile Arg Lys Phe Glu Arg Glu Leu Met Leu Glu Gln Gln Glu
174 275 280 285
175 Met Leu Met Gly Glu Lys Gln Val Ile Leu Gln Arg Gln Gln Glu Glu
176 290 295 300
177 Ile Ser Arg Leu Met His Ile Gln Lys Asn Ala Asp Cys Thr Ser Phe
178 305 310 315 320
179 Ser Glu Leu Val Glu Asn Phe Lys Lys Thr Leu Ser His Thr Asp Pro
180 325 330 335
181 Met Val Leu Asp Asp Phe Gly Thr Ser Leu Pro Phe Ile Asp Ile Tyr
182 340 345 350

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```

183 Phe Ser Thr Leu Asp Tyr Gln Asp Thr Thr Val His Lys Leu Gln Glu
184           355           360           365
185 Leu Tyr Tyr Glu Ile Val His Val Leu Ser Leu Met Leu Glu Asp Leu
186           370           375           380
187 Pro Gln Glu Lys Pro Gln Ser Leu Glu Lys Val Asp Glu Lys
188 385           390           395
190 <210> SEQ ID NO: 3
191 <211> LENGTH: 1197
192 <212> TYPE: DNA
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 3
196 atgtctcaac accgtcacca gcgccactcg agagtcattt ctagtccacc agttgacact      60
197 acatcggtgg gattttgccc aacattcaag aaattttaaga ggaacgatga tgaatgtcgg      120
198 gcatttgtga agagagtcac aatgagccgt ttctttaaga taattatgat tagcactgtc      180
199 acatcgaatg cgttttttat ggccttgtgg accagttatg acataaggta ccgcttggtc      240
200 agacttcctg agttctcgga gatcttcttt gtgtccatct gcacatctga gttgtccatg      300
201 aagggtctatg tggaccccat caactactgg aagaacggct acaacctgct ggatgtgatc      360
202 attatcatcg ttatgttttt accctatgcc ctccgccagc tcatgggcaa acagttcact      420
203 tacctgtata tcgctgatgg catgcagtcc ctgcgcaccc tcaagcttat cggctatagc      480
204 cagggcatcc ggacgctgat caccgccgtg gggcagacag tctacaccgt ggcctctgtg      540
205 ctccctcctg ccttccctcct catgtacatc ttcgctatct tgggcttctg cctgttttga      600
206 tctccagaca atggtgacca tgataactgg gggaacctgg ctgcagcttt ttccaccctc      660
207 ttcagcttgg ccacggttga tggctggaca gacctgcaga agcagttgga caatcgggaa      720
208 tttgtcttga gccgggcatt caccatcatc ttcatcttgc tcgcctcttt catcttcttc      780
209 aacatgttcg tgggtgtgat gatcatgcac acagaggact ccatcagaaa gtttgagcga      840
210 gagctgatgt tggagcagca ggagatgctc atgggagaga agcaggtgat tctgcagcgg      900
211 cagcaggagg agatcagcag gctgatgcac atacagaaaa atgctgactg cacaagtttc      960
212 agtgagctgg tggagaactt taagaagacc ttgagccaca ctgacccaat ggtcttggat      1020
213 gattttggca ctagcttacc cttcategat atctactttt cactcttgga ctaccaggac      1080
214 acaactgtcc acaagcttca agagctgtac tatgagatcg tgcagtgtgct gagcctaagt      1140
215 ctggaagact tgccccagga gaagccccag tccttggaag aggtggatga gaagtag      1197
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 305
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: consensus sequence
225 <400> SEQUENCE: 4
226 Ile Val Ser Ser Pro Tyr Phe Glu Leu Phe Ile Leu Leu Thr Ile Leu
227 1           5           10           15
228 Leu Asn Asp Asp Lys Val Ser Lys Thr Ile Ala Leu Ala Met Glu His
229           20           25           30
230 Pro Asn Gln Glu Thr Leu Asn Asp Ile Leu Asp Tyr Val Glu Tyr Val
231           35           40           45
232 Phe Thr Gly Ile Phe Thr Phe Glu Met Leu Leu Lys Met Ile Ala Leu
233           50           55           60
234 Gly Phe Lys Leu His Lys Gly Ala Tyr Phe Arg Asn Gly Trp Asn Ile
235 65           70           75           80
236 Leu Asp Phe Val Val Val Leu Leu Ser Ile Ile Glu Leu Gly Leu Ser

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```

237          85          90          95
238 Leu Ile Asn Lys Lys Ala Ala Asn Val Gly Gly Ser Pro Gln Gln Ala
239          100          105          110
240 Lys Gly Ser Leu Phe Gly Leu Lys Val Leu Arg Leu Phe Arg Val Leu
241          115          120          125
242 Arg Pro Leu Lys Leu Val Arg Arg Ala Pro Gly Leu Arg Val Leu Val
243          130          135          140
244 Gln Thr Leu Leu Asn Ser Met Lys Ala Leu Gly Asn Leu Leu Leu Leu
245 145          150          155          160
246 Leu Phe Leu Phe Val Phe Ile Phe Ala Ile Ile Gly Met Gln Leu Phe
247          165          170          175
248 Ala Gly Lys Phe Glu Phe Asp Cys Ile Asp Glu Ser Thr Glu Leu Phe
249          180          185          190
250 Asp Ile Ile Ala Thr Glu Pro Ser Leu Cys Gly Asn Glu Ser Tyr Ala
251          195          200          205
252 Arg Asp Cys Pro Asp Gly Tyr Thr Cys Arg Arg Gly Trp Glu Gly Pro
253          210          215          220
254 Asn Asn Gly Arg Thr Asn Phe Asp Asn Phe Pro Gln Ala Phe Leu Thr
255 225          230          235          240
256 Leu Phe Gln Val Met Thr Gly Glu Gly Trp Gly Asp Val Leu Tyr Asp
257          245          250          255
258 Thr Ile Asp Ala Ala Gly Glu Asp Cys Asp Pro Glu Ser Glu Ala Gly
259          260          265          270
260 Gly Gly Ile Cys Gly Asn Asn Val Leu Met Gly Ile Tyr Phe Ile Ser
261          275          280          285
262 Leu Ile Ile Leu Gly Ser Phe Leu Thr Leu Asn Leu Phe Leu Ala Val
263          290          295          300
264 Ile
265 305
267 <210> SEQ ID NO: 5
268 <211> LENGTH: 1836
269 <212> TYPE: PRT
270 <213> ORGANISM: Homo sapiens
272 <400> SEQUENCE: 5
273 Met Ala Arg Pro Ser Leu Cys Thr Leu Val Pro Leu Gly Pro Glu Cys
274 1          5          10          15
275 Leu Arg Pro Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Gln Arg Ala
276          20          25          30
277 Val Glu Glu Glu Ala Arg Leu Gln Arg Asn Lys Gln Met Glu Ile Glu
278          35          40          45
279 Glu Pro Glu Arg Lys Pro Arg Ser Asp Leu Glu Ala Gly Lys Asn Leu
280          50          55          60
281 Pro Met Ile Tyr Gly Asp Pro Pro Pro Glu Val Ile Gly Ile Pro Leu
282 65          70          75          80
283 Glu Asp Leu Asp Pro Tyr Tyr Ser Asn Lys Lys Thr Phe Ile Val Leu
284          85          90          95
285 Asn Lys Gly Lys Ala Ile Phe Arg Phe Ser Ala Thr Pro Ala Leu Tyr
286          100          105          110
287 Leu Leu Ser Pro Phe Ser Val Val Arg Arg Gly Ala Ile Lys Val Leu

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/875,363

DATE: 06/21/2001

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Input Set : A:\10448-060001.TXT

Output Set: N:\CRF3\06212001\I875363.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6